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Date: <b>September 07, 2005</b>	Client & Matter Number: <b>018547-004131US</b>	No. Pages (Including this one): <b>3</b>
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From: Joe Liebeschuetz, Reg. No. 37,505		(0229)

**Message:**

Re: U.S. Application Serial No. 09/510,378  
For: Arrays of Nucleic Acid Probes on Biological Chips  
Filed February 22, 2000  
Customer No. 20350  
Confirmation No. 3064  
Attorney Docket No. 018547-004131US

An outline for interview of 09/510,378 on Thursday September 8 follows.  
(This is not an official communication.)

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Outline for interview of 09/510,378 on Thursday September 8

Rejection of claim 82 under 35 USC 112, second paragraph

Claim 82. (previously presented) A method of comparing a target nucleic acid with a reference sequence comprising a predetermined sequence of nucleotides, the method comprising:

(a) hybridizing a sample comprising the target nucleic acid to an array of oligonucleotide probes immobilized on a solid support, the array comprising:

(1) a first probe set comprising a plurality of different probes, each probe exactly complementary to a subsequence of the reference sequence, the probe including a single interrogation position complementary to a corresponding nucleotide in the reference sequence, wherein the reference sequence is at least 50 bases, and the different probes of the first probe set are overlapping probes spanning the reference sequence;

(2) a second probe set comprising a corresponding probe for each of the different probes in the first probe set, the corresponding probe in the second probe set being identical to the corresponding probe from the first probe set that includes the interrogation position, except that the one interrogation position is occupied by a different nucleotide in each of the two corresponding probes from the first and second probe sets;

wherein, the different probes in the first probe set have at least three interrogation positions respectively corresponding to each of at least three contiguous nucleotides in the reference sequence, and

(b) detecting a hybridization pattern of the oligonucleotide probes to the target nucleic acid and determining from the hybridization pattern whether a nucleotide in the target sequence is the same or different from the corresponding nucleotide in the reference sequence.

Applicant's position

(a) The reference to a "single" interrogation position in clause (1) is not inconsistent with the reference to "at least three interrogation positions" in the "wherein" clause because the former is

referring to a property of each individual probe, and the latter to the property of the different probes collectively.

(b) It is unreasonable to insist on reading the "wherein" clause in a manner that is inconsistent with clause (1).

(c) The intended meaning of the claim is clear from the file history.

(d) The definiteness requirement does not require absolute definiteness, only that persons skilled in the art are reasonably apprised of the scope of the claim. *Shatterproof Glass Corp. v. Libbey-Owens Ford Co.*, 225 USPQ 633, 641 (Fed. Cir. 1985). "[I]f the language used by applicant satisfies the statutory requirement of 35 USC 112, second paragraph, but the examiner merely wants the applicant to improve the clarity or precision of the language used, the claims must not be rejected under 35 USC 112, second paragraph, rather the examiner should suggest improved language to the applicant." MPEP 2173.02.

(e) Applicants would be willing to insert "collectively" in the "wherein" clause as a clarification but this has been rejected as new matter "wherein, the different probes in the first probe set collectively have at least three interrogation positions respectively corresponding to each of at least three contiguous nucleotides in the reference sequence," but this has been rejected as new matter.